



## SEQUENCE LISTING

<110> KELER, TIBOR  
GOLDSTEIN, JOEL  
GRAZIANO, ROBERT  
DEO, YASHWANT M.

<120> CELLS EXPRESSING ANTI-FC RECEPTOR BINDING COMPONENTS

<130> CDJ-099CN

<140> 10/764,131

<141> 2004-01-23

<150> 09/203,958

<151> 1998-12-02

<150> 60/067,232

<151> 1997-12-02

<160> 5

<170> PatentIn Ver. 3.3

<210> 1

<211> 1132

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
construct

<220>

<221> CDS

<222> (74)..(1129)

<400> 1

aagcttggtga ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggcctt 60

ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109  
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu  
1 5 10

ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157  
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp  
15 20 25

tat gct ggg gcc cag ccg gcc aga tct gat atc cag ctg acc cag agc 205  
Tyr Ala Gly Ala Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser  
30 35 40

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 253  
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys  
45 50 55 60

aag tcc agt caa agt gtt tta tac agt tca aat cag aag aac tac ttg	301
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu	
65 70 75	
gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc tac	349
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr	
80 85 90	
tgg gca tcc act agg gaa tct ggt gtg cca agc aga ttc agc ggt agc	397
Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser	
95 100 105	
ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca gag	445
Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu	
110 115 120	
gac atc gcc acc tac tac tgc cat caa tac ctc tcc tcg tgg acg ttc	493
Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe	
125 130 135 140	
ggc caa ggg acc aag gtg gaa atc aag agc tct ggc ggt ggc ggc tcc	541
Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Ser	
145 150 155	
gga ggt gga ggc agc gga ggg ggt gga tcc gag gtc caa ctg gtg gag	589
Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu	
160 165 170	
agc ggt gga ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc	637
Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys	
175 180 185	
tcc tcg tct ggc ttc att ttc agt gac aat tac atg tat tgg gtg aga	685
Ser Ser Ser Gly Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg	
190 195 200	
cag gca cct gga aaa ggt ctt gag tgg gtt gca acc att agt gat ggt	733
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly	
205 210 215 220	
ggt agt tac acc tac tat cca gac agt gtg aag gga aga ttt aca ata	781
Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile	
225 230 235	
tcg aga gac aac agc aag aac aca ttg ttc ctg caa atg gac agc ctg	829
Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu	
240 245 250	
aga ccc gaa gac acc ggg gtc tat ttt tgt gca aga ggc tac tat agg	877
Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg	
255 260 265	
tac gag ggg gct atg gac tac tgg ggc caa ggg acc ccg gtc acc gtc	925
Tyr Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val	
270 275 280	

```

tcc tca ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa gag 973
Ser Ser Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu
285 290 295 300

gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg cca 1021
Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro
305 310 315

cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc ctg 1069
His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu
320 325 330

gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg cag 1117
Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln
335 340 345

aag aag cca cgt tag 1132
Lys Lys Pro Arg
350

<210> 2
<211> 1135
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
construct

<220>
<221> CDS
<222> (74)..(1132)

<400> 2
aagccttgta ccgagctcgg atccactagt aacggcgccc agtgtgctgg aattcggtt 60
1 5 10

ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
1 5 10

ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
15 20 25

tat gct ggg gcc cag ccg gcc aga tct gag atc cag ctg cag cag act 205
Tyr Ala Gly Ala Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr
30 35 40

gga cct gag ctg gtg aag cct ggg gct tca gtg aag ata tcc tgc aag 253
Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys
45 50 55 60

gct tct ggt tat tca ttc act gac tac atc ata ttt tgg gtg aag cag 301
Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln
65 70 75

```

agc cat gga aag agc ctt gag tgg act gga aat att aat cct tac tat	349
Ser His Gly Lys Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr	
80 85 90	
ggt agt act agc tac aat ctg aag ttc aag ggc aag gcc aca ttg act	397
Gly Ser Thr Ser Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr	
95 100 105	
gta gac aaa tct tcc agc aca gcc tac atg cag ctc aac agt ctg aca	445
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr	
110 115 120	
tct gag gac tct gca gtc tat tac tgt gta aga gga gtt tat tac tac	493
Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr	
125 130 135 140	
ggt agt agc tac gag gcg ttt cct tac tgg ggc caa ggg act ctg gtc	541
Gly Ser Ser Tyr Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val	
145 150 155	
act gtc tct gca gga ggt ggc ggc tcc gga gga ggt ggc agc gga ggg	589
Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly	
160 165 170	
ggc gga tcc gat gtt gtg atg acc cag act cca ctc act ttg tgc att	637
Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile	
175 180 185	
acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc	685
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu	
190 195 200	
tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca	733
Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro	
205 210 215 220	
ggc cag tct cca acg cgc cta atc tat ctg gtg tct aaa ctg gac tct	781
Gly Gln Ser Pro Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser	
225 230 235	
gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca	829
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr	
240 245 250	
ctg aaa atc agc aga gtg gag gct gag gat ttg gga att tat tat tgc	877
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys	
255 260 265	
tgg caa ggt gca cat ttt cct cag acg ttc ggt gga ggc acc aag ctg	925
Trp Gln Gly Ala His Phe Pro Gln Thr Phe Gly Gly Thr Lys Leu	
270 275 280	
gaa atc aaa ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa	973
Glu Ile Lys Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu	
285 290 295 300	

gag gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg 1021  
 Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val  
 305 310 315

cca cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc 1069  
 Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala  
 320 325 330

ctg gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg 1117  
 Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp  
 335 340 345

cag aag aag cca cgt tag 1135  
 Gln Lys Lys Pro Arg  
 350

<210> 3

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 3

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala  
 20 25 30

Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu  
 35 40 45

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln  
 50 55 60

Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln  
 65 70 75 80

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr  
 85 90 95

Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 100 105 110

Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr  
 115 120 125

Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gln Gly Thr  
 130 135 140

Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 145 150 155 160

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly  
 165 170 175  
 Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ser Ser Gly  
 180 185 190  
 Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly  
 195 200 205  
 Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly Gly Ser Tyr Thr  
 210 215 220  
 Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
 225 230 235 240  
 Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp  
 245 250 255  
 Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg Tyr Glu Gly Ala  
 260 265 270  
 Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Pro Arg  
 275 280 285  
 Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala  
 290 295 300  
 Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro  
 305 310 315 320  
 Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr  
 325 330 335  
 Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg  
 340 345 350  
  
 <210> 4  
 <211> 353  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 construct  
  
 <400> 4  
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala  
 20 25 30  
 Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr Gly Pro Glu Leu  
 35 40 45  
 Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr  
 50 55 60

Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln Ser His Gly Lys  
 65 70 75 80  
 Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr Gly Ser Thr Ser  
 85 90 95  
 Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser  
 100 105 110  
 Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser  
 115 120 125  
 Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr Gly Ser Ser Tyr  
 130 135 140  
 Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 145 150 155 160  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp  
 165 170 175  
 Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile Thr Ile Gly Gln  
 180 185 190  
 Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp  
 195 200 205  
 Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro  
 210 215 220  
 Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp  
 225 230 235 240  
 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser  
 245 250 255  
 Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Ala  
 260 265 270  
 His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Pro  
 275 280 285  
 Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 290 295 300  
 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu  
 305 310 315 320  
 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu  
 325 330 335  
 Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro  
 340 345 350  
 Arg

<210> 5  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 5  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15